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<110> Matsumoto, Hirokazu

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<150> JP 9-165437

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TGGTACGCRG GCCGTGGGAT CCGGCCCGTG GGCCGCTTCG GCCGGCGAAG AGCTGCCCCY 180
GGGGACGGAC CCAGGCCTGG CCCCCGGCGT GTGCCGGCCT GCTTCCGCCT GGAAGGCGGY 240
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Val Gly Arg Phe
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<211> 93

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 20 25 30
 Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
 35 40 45
 Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr
 50 55 60
 Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
 65 70 75 80
 Val Val Leu Val His Pro Leu Arg Arg Arg Ile
 85 90

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 20 25 30
 Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg
 35 40 45
 Thr Phe Cys Leu Leu Val Val Val Val Val Val
 50 55

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 <400> 21

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 20 25 30
 Ser Ala Gly Asn Gly Ser Val Ala Gly Ala Asp Ala Pro Ala Val Thr
 35 40 45
 Pro Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Gly Leu Ile Val
 50 55 60
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 65 70 75 80
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Cys	Val	Pro 35	Leu	Thr	Leu	Ala	Tyr 40	Ala	Phe	Glu	Pro	Arg 45	Gly	Trp	Val
Phe	Gly 50	Gly	Gly	Leu	Cys	His 55	Leu	Val	Phe	Phe	Leu 60	Gln	Ala	Val	Thr
Val 65	Tyr	Val	Ser	Val	Phe 70	Thr	Leu	Thr	Thr	Ile 75	Ala	Val	Asp	Arg	Tyr 80
Val	Val	Leu	Val	His 85	Pro	Leu	Arg	Arg	Arg 90	Ile	Ser	Leu	Arg	Leu	Ser 95
Ala	Tyr	Ala	Val 100	Leu	Ala	Ile	Trp	Val 105	Leu	Ser	Ala	Val	Leu 110	Ala	Leu
Pro	Ala	Ala 115	Val	His	Thr	Tyr	His 120	Val	Glu	Leu	Lys	Pro 125	His	Asp	Val
Arg	Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Leu

130 135 140
Tyr Ala Trp Gly Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
145 150 155 160
Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu Arg Asn Arg Val
165 170 175
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195 200 205

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20 25 30
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35 40 45
Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Ile
50 55 60
Tyr Ala Trp Gly Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala
65 70 75 80
Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val
85 90 95
Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
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GCCTTCGAGC CACGCGGCTG GGTGTTTCGGC GGCGGCCTGT GCCACCTGGT CTTCTTCCTG 180
CAGCCGGTCA CCGTCTATGT GTCGGTGTTC ACGCTCACCA CCATCGCAGT GGACCGGTAC 240
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GGCGCGGACG CTCCAGCCGT CACGCCCTTC CAGAGCCTGC AGCTGGTGCA TCAGCTGAAG 180
GGGTGATCG TGCTGCTCTA CAGCGTCGTG GTGGTCGTGG GGCTGGTGGG CAACTGCCCTG 240
CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGCACAACG TGACGAACCTT CCTCATCGGC 300
AACCTGGCCT TGTCCGACGT GCTCATGTGC ACCGCTGCG TGCCGCTCAC GCTGGCCTAT 360
GCCTTCGAGC CACGCGGCTG GGTGTTCCGG GCGGCTGTGT GCCACCTGGT CTTCTTCCCTG 420
CAGCCGGTCA CCGTCTATGT GTCGGTGTTC ACGCTACCA CCATCGCAGT GGACCGCTAC 480
GTGTGCTGG TGCAACCGCT GAGGCGGCGC ATCTCGCTGC GCCTCAGCGC CTACGCTGTG 540
CTGGCCATCT GGGCGCTGTC CGCGGTGCTG GCGCTGCCCG CCGCCGTGCA CACCTATCAC 600
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CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACCTGCTCCC TCTGCTGGTC 720
ATCCTCCTGT CTTACGTCCG GGTGTCACTG AAGCTCCGCA ACCGCGTGGT GCCGGGCTGC 780
GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGCACCTT CTGCTTGCTG 840
GTGGTGGTGG TGGTGGTGGT CGCCGTCTGC TGGCTGCCCG TGCAAGTCTT CAACCTGCTG 900
CGGGACCTCG ACCCCACCGC CATCGACCCT TACGCTTTG GGCTGGTGCA GCTGCTCTGC 960
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ATCCTCCTGT CTTACGCCCC GGTGTCACTG AAGCTCCGCA ACCGCGTGGT GCCGGGCGC 540
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GTGGAGCTCA AGCCCCACGA CGTGAGCCTC TGCGAGGAGT TCTGGGGCTC GCAGGAGCGC 180
CAACGCCAGA TCTACGCCTG GGGGCTGCTT CTGGGCACCT ATTTGCTCCC CCTGCTGGCC 240
ATCCTCCTGT CTTACGTACG GGTGTCAGTG AAGCTGAGGA ACCGCGTGGT GCCTGGCAGC 300
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<210> 31

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<210> 36

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<210> 38

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 20 25 30
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 35 40 45
 Pro Val Gly Arg Phe Gly Arg Arg Ala Ala Leu Gly Asp Gly Pro
 50 55 60
 Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly
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 Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val
 85 90 95
 Gln Glu

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 <400> 45

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 20 25 30
 Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
 35 40 45
 Val Gly Arg Phe Gly Arg Arg Arg Ala Thr Pro Arg Asp Val Thr Gly
 50 55 60
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 Gln Arg Gly

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 <400> 46

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 TACACGGGCC GCGGGATCAG GCCTGTGGGC CGCTTCGGCA GGAGAAGGGC AACCCCGAGG 180
 GATGTCACTG GACTTGGCCA ACTCAGCTGC CTCCCACTGG ATGGACGGAC CAAGTTCTCT 240
 CAGCGTGGA 249

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 20 25 30

<210> 48
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 <213> Rat
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 1 5 10 15
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 20 25 30

<210> 49
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 <213> Rat
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Arg 20 25 30

<210> 50
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 <212> PRT
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 1 5 10 15
 Val Gly Arg Phe
 20

<210> 51
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 <400> 51

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 1 5 10 15
 Val Gly Arg Phe Gly
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 1 5 10 15
 Val Gly Arg Phe Gly Arg
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<210> 57

<211> 63

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<210> 58

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<211> 87

<212> PRT

<213> Human

<400> 59

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20 25 30
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg
35 40 45
Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Thr Leu Gly Asp Val Pro
50 55 60
Lys Pro Gly Leu Arg Pro Arg Leu Thr Cys Phe Pro Leu Glu Gly Gly
65 70 75 80
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<211> 261

<212> DNA

<213> Human

<400> 60

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TGGTACGCCA GTCGCGGGAT CAGGCCTGTG GGCCGCTTCG GTCGGAGGAG GGCAACCCCTG 180
GGGGACGTCC CCAAGCCTGG CCTGCGACCC CGGCTGACCT GCTTCCCCCT GGAAGGCGGT 240
GCTATGTCGT CCCAGGATGG C 261

<210> 61

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<213> Human

<400> 61

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1 5 10 15
Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe

<210> 62
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 <213> Human
 <400> 62

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 1 5 10 15
 Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
 20 25 30

<210> 63
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 <213> Human
 <400> 63

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 1 5 10 15
 Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
 20 25 30
 Arg

<210> 64
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 <213> Human
 <400> 64

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 1 5 10 15
 Val Gly Arg Phe
 20

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 <220>
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 Xaa of the 5th position is Gln or Arg.
 Xaa of the 10th position is Ile or Thr.

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 1 5 10

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<210> 79

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<212> DNA

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Run	Time	Temp	Pressure	Flow	Conc	Yield	Notes
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3	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
4	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
5	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
6	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
7	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
8	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
9	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
10	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
11	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
12	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
13	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
14	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
15	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
16	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
17	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
18	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
19	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
20	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
21	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
22	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
23	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
24	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
25	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
26	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
27	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
28	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
29	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
30	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
31	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
32	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
33	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
34	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
35	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
36	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
37	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
38	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
39	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
40	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
41	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
42	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
43	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
44	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
45	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
46	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
47	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
48	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
49	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
50	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
51	10.0	1					